

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/553,730
Source: PCT/IO
Date Processed by STIC: 11/1/05

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PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/553,730

DATE: 11/01/2005

TIME: 10:49:16

Input Set : A:\SEQUENCE LIST 33157A.TXT
 Output Set: N:\CRF4\11012005\J553730.raw

3 <110> APPLICANT: KUMAR, Chandrika S.
 4 DAOUTI, Sherif
 5 LATARIO, Brian J.
 7 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS TARGETING TYROSINE KINASES
 9 <130> FILE REFERENCE: 3491/0M582US0
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/553,730
 C--> 12 <141> CURRENT FILING DATE: 2005-10-14
 14 <160> NUMBER OF SEQ ID NOS: 35
 16 <170> SOFTWARE: PatentIn version 3.2
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 3949
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Homo sapiens
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 38 tggaggggat ggaggagct gacatccagt ggtgaagga tggggctgtg gtccagaact 480
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88	tcagggaagc	agcttgcatg	aaggagtttgc	accatccaca	cgtggccaaa	cttgggggg	1980											
90	taagcctccg	gagcagggtc	aaaggccgtc	tccccatccc	catggtcata	ttgccttca	2040											
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169							20			25					30			
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173							35			40					45			
176	Pro	Val	Lys	Leu	Thr	Val	Ser	Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys		

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180	Ser Val Glu Gly Met Glu Glu Pro Asp Ile Gln Trp Val Lys Asp Gly		
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184	Ala Val Val Gln Asn Leu Asp Gln Leu Tyr Ile Pro Val Ser Glu Gln		80
185	85	90	95
188	His Trp Ile Gly Phe Leu Ser Leu Lys Ser Val Glu Arg Ser Asp Ala		
189	100	105	110
192	Gly Arg Tyr Trp Cys Gln Val Glu Asp Gly Gly Glu Thr Glu Ile Ser		
193	115	120	125
196	Gln Pro Val Trp Leu Thr Val Glu Gly Val Pro Phe Phe Thr Val Glu		
197	130	135	140
200	Pro Lys Asp Leu Ala Val Pro Pro Asn Ala Pro Phe Gln Leu Ser Cys		
201	145	150	155
204	160	165	175
208	Glu Ala Val Gly Pro Pro Glu Pro Val Thr Ile Val Trp Trp Arg Gly		
209	180	185	190
212	Thr Thr Lys Ile Gly Gly Pro Ala Pro Ser Pro Ser Val Leu Asn Val		
213	195	200	205
216	Lys Gly Leu Ala Ser Ser Arg Thr Ala Thr Val His Leu Gln Ala Leu		
217	210	215	220
220	Pro Ala Ala Pro Phe Asn Ile Thr Val Thr Lys Leu Ser Ser Ser Asn		
221	225	230	235
224	240	245	255
225	Ala Ser Val Ala Trp Met Pro Gly Ala Asp Gly Arg Ala Leu Leu Gln		
228	260	265	270
232	Ser Cys Thr Val Gln Val Thr Gln Ala Pro Gly Gly Trp Glu Val Leu		
233	275	280	285
236	290	295	300
240	Val Pro Ala Thr Asn Tyr Ser Leu Arg Val Arg Cys Ala Asn Ala Leu		
241	305	310	315
244	320	325	335
245	Ala Pro Ala Ser Ala Pro Gln Asn Leu His Ala Ile Arg Thr Asp Ser		
248	340	345	350
249	Gly Leu Ile Leu Glu Trp Glu Glu Val Ile Pro Glu Ala Pro Leu Glu		
252	355	360	365
253	Gly Pro Leu Gly Pro Tyr Lys Leu Ser Trp Val Gln Asp Asn Gly Thr		
256	370	375	380
257	Gln Asp Glu Leu Thr Val Glu Gly Thr Arg Ala Asn Leu Thr Gly Trp		
260	385	390	395
261	Asp Pro Gln Lys Asp Leu Ile Val Arg Val Cys Val Ser Asn Ala Val		400
264	405	410	415
265	Gly Cys Gly Pro Trp Ser Gln Pro Leu Val Val Ser Ser His Asp Arg		
268	420	425	430
269	Ala Gly Gln Gln Gly Pro Pro His Ser Arg Thr Ser Trp Val Pro Val		
272	435	440	445
273	Val Leu Gly Val Leu Thr Ala Leu Val Thr Ala Ala Ala Leu Ala Leu		

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276 Ile Leu Leu Arg Lys Arg Arg Lys Glu Thr Arg Phe Gly Gln Ala Phe
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280 Asp Ser Val Met Ala Arg Gly Glu Pro Ala Val His Phe Arg Ala Ala
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284 Arg Ser Phe Asn Arg Glu Arg Pro Glu Arg Ile Glu Ala Thr Leu Asp
285 485 490 495
288 Ser Leu Gly Ile Ser Asp Glu Leu Lys Glu Lys Leu Glu Asp Val Leu
289 500 505 510
292 Ile Pro Glu Gln Gln Phe Thr Leu Gly Arg Met Leu Gly Lys Gly Glu
293 515 520 525
296 Phe Gly Ser Val Arg Glu Ala Gln Leu Lys Gln Glu Asp Gly Ser Phe
297 530 535 540
300 Val Lys Val Ala Val Lys Met Leu Lys Ala Asp Ile Ile Ala Ser Ser
301 545 550 555 560
304 Asp Ile Glu Glu Phe Leu Arg Glu Ala Ala Cys Met Lys Glu Phe Asp
305 565 570 575
308 His Pro His Val Ala Lys Leu Val Gly Val Ser Leu Arg Ser Arg Ala
309 580 585 590
312 Lys Gly Arg Leu Pro Ile Pro Met Val Ile Leu Pro Phe Met Lys His
313 595 600 605
316 Gly Asp Leu His Ala Phe Leu Leu Ala Ser Arg Ile Gly Glu Asn Pro
317 610 615 620
320 Phe Asn Leu Pro Leu Gln Thr Leu Ile Arg Phe Met Val Asp Ile Ala
321 625 630 635 640
324 Cys Gly Met Glu Tyr Leu Ser Ser Arg Asn Phe Ile His Arg Asp Leu
325 645 650 655
328 Ala Ala Arg Asn Cys Met Leu Ala Glu Asp Met Thr Val Cys Val Ala
329 660 665 670
332 Asp Phe Gly Leu Ser Arg Lys Ile Tyr Ser Gly Asp Tyr Tyr Arg Gln
333 675 680 685
336 Gly Cys Ala Ser Lys Leu Pro Val Lys Trp Leu Ala Leu Glu Ser Leu
337 690 695 700
340 Ala Asp Asn Leu Tyr Thr Val Gln Ser Asp Val Trp Ala Phe Gly Val
341 705 710 715 720
344 Thr Met Trp Glu Ile Met Thr Arg Gly Gln Thr Pro Tyr Ala Gly Ile
345 725 730 735
348 Glu Asn Ala Glu Ile Tyr Asn Tyr Leu Ile Gly Gly Asn Arg Leu Lys
349 740 745 750
352 Gln Pro Pro Glu Cys Met Glu Asp Val Tyr Asp Leu Met Tyr Gln Cys
353 755 760 765
356 Trp Ser Ala Asp Pro Lys Gln Arg Pro Ser Phe Thr Cys Leu Arg Met
357 770 775 780
360 Glu Leu Glu Asn Ile Leu Gly Gln Leu Ser Val Leu Ser Ala Ser Gln
361 785 790 795 800
364 Asp Pro Leu Tyr Ile Asn Ile Glu Arg Ala Glu Glu Pro Thr Ala Gly
365 805 810 815
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369 820 825 830
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376 Tyr Ile Leu Thr Pro Gly Gly Leu Ala Glu Gln Pro Gly Gln Ala Glu
377      850          855          860
380 His Gln Pro Glu Ser Pro Leu Asn Glu Thr Gln Arg Leu Leu Leu Leu
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385          885          890
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389 <211> LENGTH: 678
390 <212> TYPE: PRT
391 <213> ORGANISM: Homo sapiens
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400          20          25          30
403 Leu Pro Ala Arg Glu Ala Thr Gln Phe Leu Arg Pro Arg Gln Arg Arg
404          35          40          45
407 Ala Phe Gln Val Phe Glu Ala Lys Gln Gly His Leu Glu Arg Glu
408          50          55          60
411 Cys Val Glu Glu Leu Cys Ser Arg Glu Glu Ala Arg Glu Val Phe Glu
412 65          70          75          80
415 Asn Asp Pro Glu Thr Asp Tyr Phe Tyr Pro Arg Tyr Leu Asp Cys Ile
416          85          90          95
419 Asn Lys Tyr Gly Ser Pro Tyr Thr Lys Asn Ser Gly Phe Ala Thr Cys
420          100         105         110
423 Val Gln Asn Leu Pro Asp Gln Cys Thr Pro Asn Pro Cys Asp Arg Lys
424          115         120         125
427 Gly Thr Gln Ala Cys Gln Asp Leu Met Gly Asn Phe Phe Cys Leu Cys
428          130         135         140
431 Lys Ala Gly Trp Gly Gly Arg Leu Cys Asp Lys Asp Val Asn Glu Cys
432 145          150          155          160
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436          165          170          175
439 Ser Phe His Cys Ser Cys His Ser Gly Phe Glu Leu Ser Ser Asp Gly
440          180          185          190
443 Arg Thr Cys Gln Asp Ile Asp Glu Cys Ala Asp Ser Glu Ala Cys Gly
444          195          200          205
447 Glu Ala Arg Cys Lys Asn Leu Pro Gly Ser Tyr Ser Cys Leu Cys Asp
448          210          215          220
451 Glu Gly Phe Ala Tyr Ser Ser Gln Glu Lys Ala Cys Arg Asp Val Asp
452 225          230          235          240
455 Glu Cys Leu Gln Gly Arg Cys Glu Gln Val Cys Val Asn Ser Pro Gly
456          245          250          255
459 Ser Tyr Thr Cys His Cys Asp Gly Arg Gly Leu Lys Leu Ser Gln
460          260          265          270
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464          275          280          285
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date